>AF249738 ACCESSION:AF249738 NID: gi 8571425 gb AF249738.1 AF249738

Mus musculus Pb99 gene sequence

Length = 2127

Score =  $358 \text{ bits (910), Expect(3)} \approx 0.0$ 

Identities = 210/293 (72%), Positives = 233/293 (80%)

Frame = +1

Query: 206 RPPPNMTLTCVFWDVTKGTTGDWSSEGCSTEVRPEGTVCCCDHLTFFALLLRPTLDQSTV 265 R P N+ LTCVFWD+ KG DW S CST TVC CDHLTFFALLLRP LD +T

Sbjct: 748 RSPHNVILTCVFWDMAKG---DWDSH-CSTVPGDGRTVCRCDHLTFFALLLRPILDLATA 915

Query: 266 HILTRISQAGCGVSMIFLAFTIILYAFLRLSRERFKSEDAPKIHVALGGSLFLLNLAFLV 325

LTRISQAG VSMIFLAFT++LY R S +RFKSEDAPKIH+AL SLFLLNL FL

Sbjct: 916 QTLTRISQAGSAVSMIFLAFTMVLYVAFRFSLQRFKSEDAPKIHMALSISLFLLNLTFLI 1095

Query: 326 NVGSGSKGSDAACWARGAVFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLV 385

NVGS S+G A+CW R A+FHYFLLC FTWMGLEAFHLYLLA+RVFNTYFGHYFLKLSL+

Sbjct: 1096 NVGSSSQGPPASCWVRAAIFHYFLLCVFTWMGLEAFHLYLLAIRVFNTYFGHYFLKLSLL 1275

Query: 386 GWGLPALMVIGTGSANSYGLYTIRDRENRTSLELCWFREGTTMYALYITVHGYFLITFLF 445

WGLP L+VIG GS+NSYG+YTIRD+ENRTSLELCWF++ ALY TVHGYFL+TFLF

Sbjct: 1276 AWGLPVLVVIGAGSSNSYGVYTIRDQENRTSLELCWFQKEP---ALYATVHGYFLVTFLF 1446

Query: 446 GMVVLALVVWKIFTLSRATAVKERGKNRKKVLTLLGLSSLVGVTWGLAIFTPL 498

G VVLALV WKIFTL TA K +G K VLT+LGLSSLVG+TWGLA+ TPL

Sbjct: 1447 GAVVLALVAWKIFTLPSVTAGKGQGPTWKSVLTVLGLSSLVGMTWGLAVLTPL 1605

Score = 245 bits (618), Expect(3) = 0.0

Identities = 129/215 (60%), Positives = 159/215 (74%), Gaps = 2/215 (0%)

Frame = +2

Query: 1 MATPRGLGALLLLLLPTSGQEKPTEGPRNTC--LGSNNMYDIFNLNDKALCFTKCRQSG 58

MAT R LG L LLL + E+ TE PRN C L + YD F+LND A CFTKC OS

Sbjct: 17 MATARSLGLLFFLLL---TSDEETTEEPRNVCRRLQEGHEYDTFDLNDTAQCFTKCGQSE 187

Query: 59 SDSCNVENLQRYWLNYEAHLMKEGLTQKVNTPFLKALVQNLSTNTAEDFYFSLEPSQVPR 118

C+V NLQRYWLNYE++L++ + + V+ PF+KAL+QN+ST+ +ED +SL SQ+PR

Sbjct: 188 HSPCDVGNLQRYWLNYESYLLENSM-ETVDMPFVKALIQNISTDVSEDLLYSLMLSQIPR 364

Query: 119 QVMKDEDKPPDRVRLPKSLFRSLPGNRSVVRLAVTILDIGPGTLFKGPRLGLGDGSGVLN 178

QVM+ ED+P D VRLPKSLF +LPGNRS VRLA+T+LDIG G +FKGP+L GS VLN

Sbjct: 365 QVMQGEDEPADGVRLPKSLFGALPGNRSAVRLAITVLDIGAGNVFKGPKLLEDKGSSVLN 544

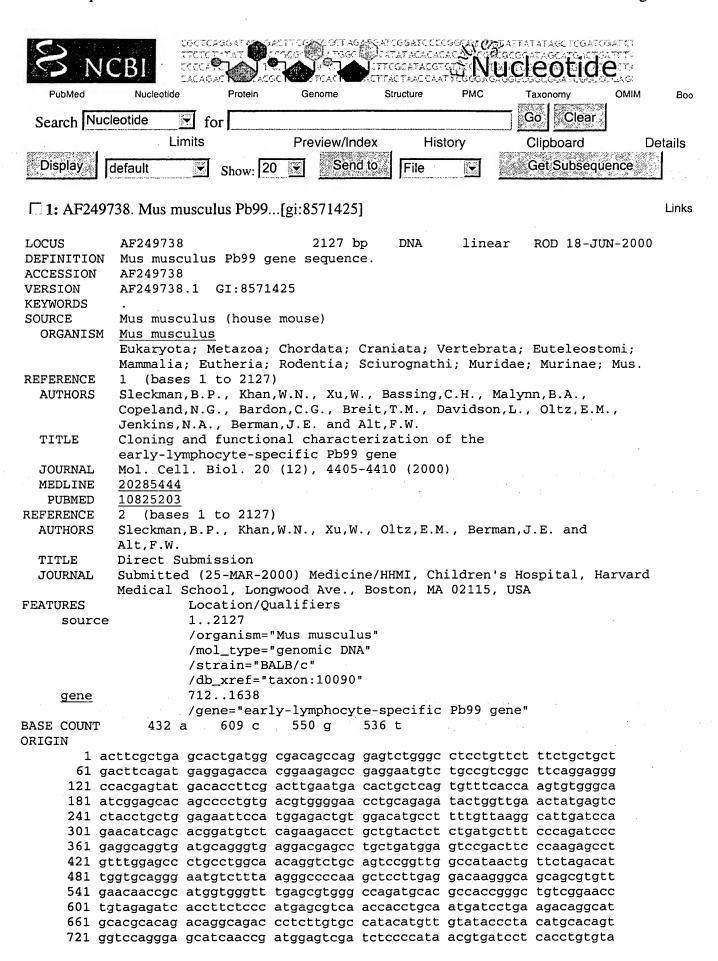
Query: 179 NRLVGLSVGQMHVTKLAEPLEIVFSHQRPPPNMTL 213

NR+VGLSVGOMH T L+EP+EI FSH+R PP M L

Sbjct: 545 NRMVGLSVGQMHATGLSEPVEITFSHERQPPAMIL 649

Score = 84.7 bits (206), Expect(3) = 0.0 Identities = 41/54 (75%), Positives = 45/54 (82%), Gaps = 1/54 (1%) Frame = +3

Query: 497 PLGLSTVYIFALFNSLQGVFICCWFTILYLPSQSTTVSSS-TARLDQAHSASQE 549
P GLST+Y+F L NSLQG+FI CWF ILY P+QSTT SSS TARLDQAHS SQE
Sbjct: 1599 PPGLSTIYVFTLLNSLQGLFIFCWFIILYFPTQSTTASSSGTARLDQAHSVSQE 1760



11

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781 ttctgggata tggctaaagg agactgggat tcccactgct ccacggtgcc cggggatggg
 841 agaactgtct gccgttgcga ccacttgacc ttcttcgcct tgctgctgag gccgatcttg
 901 gacctggcca cggcacagac teteactege ateteceagg caggeagtge egtetecatg
 961 atetteetgg cetteaceat ggtgetetat gttgeettea ggttetetet geagaggtte
1021 aagtotgaag atgoccotaa gatocacatg gototgagca toagcotgtt totootgaat
1081 cttacettee tgateaatgt ggggageage teccaaggee ceccageete etgetgggte
1141 cgagctgcca ttttccacta ctttctgctc tgtgtcttca cctggatggg tctggaggcc
1201 ttccacctct acctgctggc catcagagtc ttcaatacct actttggaca ctatttcctq
1261 aagctgagcc tgctggcctg gggcctgcct gttcttgtag ttattggtgc tggaagtagc
1321 aacagttatg gagtttacac cattcgcgac caggagaacc gcacatcact ggagttgtgc
1381 tggttccaga aagagcctgc tctttatgct actgtccacg gctacttcct tgttaccttc
1441 ctcttcggtg ctgtggtact ggctttggtg gcctggaaga tcttcactct gcccagtgtc
1501 acagegggca aaggacaggg geegacetgg aagteggtee teacegtget gggeetetee
1561 agtctggtgg gcatgacctg ggggctggct gttctcaccc ccctggcttg tctaccatct
1621 acgtetteae cetettaaae tetetaeaag ggetetteat ettetgetgg tteateatee
1681 tetaetteec tacteagage accaeageet ceteeteegg cacegeeege etggaceagg
1741 cccactccgt gtcccaggag tagatgatgg gtggctgcag tttgctctca cttctggctg
1801 gtttgtgtga ccttgaacag ctccctactt ccttctgggc tccactgtct tctctgtaca
1861 ggatgtccaa ggacggagag ggtgaggacc aagccaggcc ctgtggcttc aaagttccca
1921 ttcaggaggc tggagacttg acttgaagag gacactggtt cagttcccag cacccacata
1981 acatetetea getgtetgtg actetagtte caagagatet gacgetgtee tetggtetee
2041 aaagagtacc aggcatgaat gtgctggata tatacatgtg ccactcatac atataaaata
2101 gaaattaaaa aaaatatttt aacagct
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